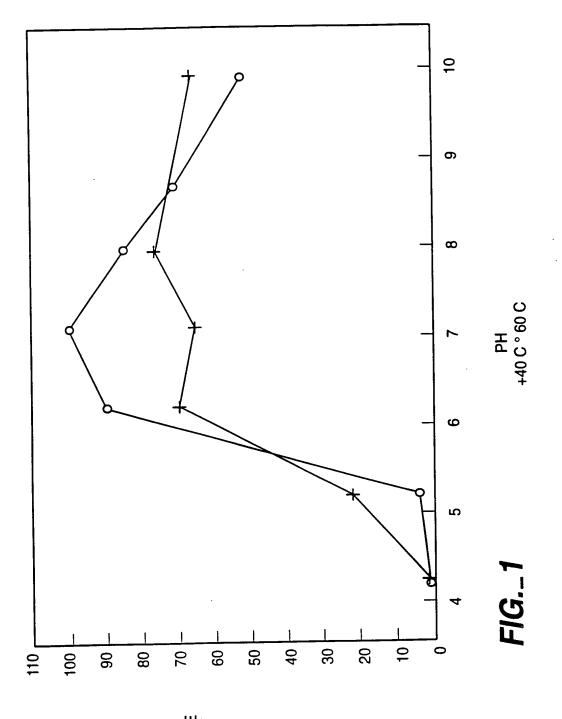
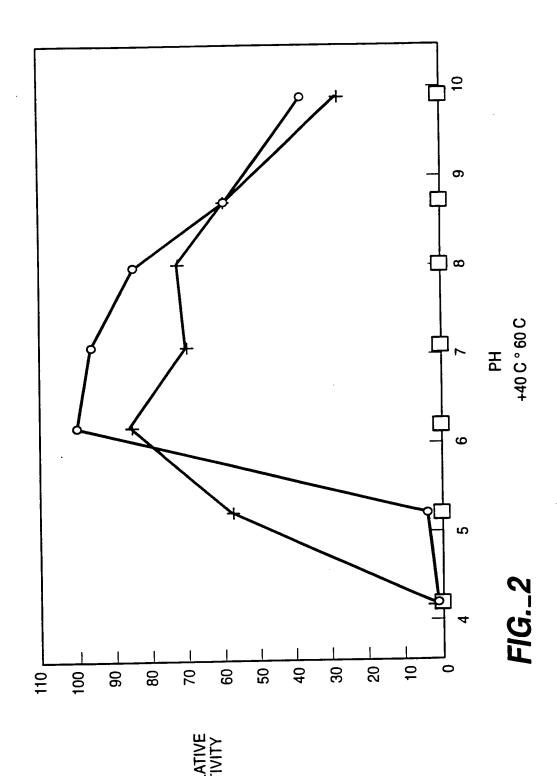
## 6313081



RELATIVE ACTIVITY

SUBSTITUTE SHEET (RULE 26)

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SUBSTITUTE SHEET (RULE 26)

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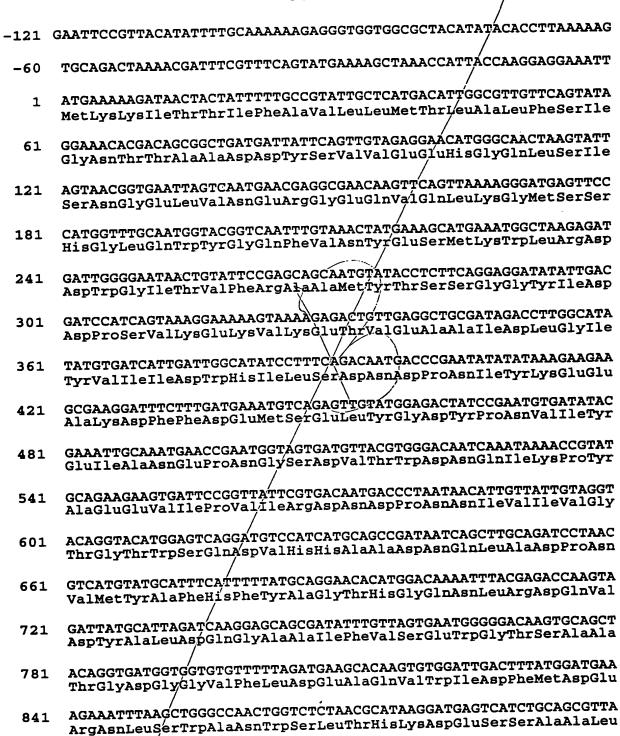


FIG.\_3A

 ${\tt ATGCCAGGT'GCAAATCCAACTGGTGGTTGGACAGAGGCTGAACTATCTCCATCTGGTACA}$ 

 ${\tt MetProGl\'yAlaAsnProThrGlyGlyTrpThrGluAlaGluLeuSerProSerGlyThr}$ 



FIG.\_3B

-630

GAATTCTTTGGATCATGATGGAAGGCGAAA

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-600	TCATGAGCATTGCCCTTGCGACGATTACGGCTTCTGTCGGCGTCTACTTGCTTG
-540	CGGTTCAAGGTTGCTTTGCAGGTAAAGCTGCATTAACTGTTGTTCGTTTACTTCTCATTC
-480	TCGCTGCTGTTTGTCTTATTCATTCAAATTGGGTGTATGACTTTGTCGCCCTCGGNATCG
-420	CGGGTATCGCCATTATNCTTCAAAGAACAGTTATTAACAGACGCCATGGGTTCCAAGGCA
-360	AGTACAGTTTAAAACGAGAGATTTAAGAGGCCGCTCCCAATGAGGGAGTGGTCTTTTTTA
-300	CATTCNAAAAAGAGGAAAATAGGAGAAATGTAGATCCGACGTAGATAAGTATTAGGTTTT
-240	AAGTGTAAGTACAGCTAAGAAAGCTGCTTTTGCTGATTCTATGAAAAAGTGCTTGTTAAA
-180	CATTTTGACATGATTTTCTGTGAAATAAATGATCTATTTTCTGTGAAACAATTGTGATAG
-120	ATTGGTGTAGAGTTTTGATAATTCTAAATTTTCGTTCAAAAGGAGGTTGAGGTTCATTTA
-60	CGATTTTGTCAACAGTCAATTGTTGTTTCCGGGTAACTCATTTGGAGGTGGTGGAGTCTG
1	ATGAAGTGGATGAAATCCATGGTATGGTTGGCCGTTGTTTTGGTCGTTCGT
	MetLysTrpMetLysSerMetValTrpLeuAlaValValLeuValValSerPheValAla
61	CCTGCCGTTAGTTCAGCTAATGAGGATGTAAAAACTCTCGATATTCAGTCCTATGTAAGA ProAlaValSerSerAlaAsnGluAspValLysThrLeuAspIleGlnSerTyrValArg
121	GACATGCAGCCGGGTTGGAATCTTGGGAATACGTTTGATGCCGTCGGACAAGATGAAACA
	AspMetGlnProGlyTrpAsnLeuGlyAsnThrPheAspAlaValGlyGlnAspGluThr
181	GCATGGGGAAATCCACGTGTGACACGAGAATTAATTGAACGGATTGCGGATGAAGGGTATAATTPGlyAsnProArgValThrArgGluLeuIleGluArgIleAlaAspGluGlyTyr
241	AAAAGCATTCGGATTCCGGTGACGTGGGAAAATCGTATCGGAGGGGCACCTGATTATCCT
<b>44</b>	LysSerIleArgIleProValThrTrpGluAsnArgIleGlyGlyAlaProAspTyrPro
301	ATTGATCCCCAGTTTTTAAATCGAGTGGACGAAGTTGTTCAATGGGCGCTGGAAGAAGATIleAspProGlnPheLeuAsnArgValAspGluValValGlnTrpAlaLeuGluGluAsp
361	TTGTATGTCATGATTAATTTACACCATGATTCATGGTTATGGATTTATGAAATGGAGCAC
301	LeuTyrValMetIleAsnLeuHisHisAspSerTrpLeuTrpIleTyrGluMetGluHis
421	AACTACAACGGTGTGATGGCCAAGTATCGCTCGCTCTGGGAGCAACTATCGAACCACTTCAASTYTASTGIyValMetAlaLysTyrArgSerLeuTrpGluGlnLeuSerAsnHisPhe
481	AAAGACTATCCAACAAAGCTTATGTTTGAAAGTGTCAATGAGCCAAAGTTTAGTCAAAAC LysaspTyrProThrLysLeuMetPheGluSerValasnGluProLysPheSerGlnAsn
541	TGGGGTGAGATCCGTGAGAATCACCATGCGTTACTAGACGACTTAAACACAGTGTTTTTCTTTTCTTTTTTTT
601	GAGATTGTGAGACAGTCTGGTGGCCAAAATGATATCCGGCCGTTAGTGTTACCGACTATGGluIleValArgGlnSerGlyGlyGlnAsnAspIleArgProLeuValLeuProThrMet
661	GAAACAGCCACATCACAACCGTTGCTGAACAACCTTTATCAAACAATTGACAAATTGGATGITTATCAAACAATTGACAAATTGGATGITTATCAAACAATTGACAAATTGGATGITTATCAAACAATTGACAAATTGGATGITTATCAAACAATTGACAAATTGGATGATAAACAATTGACAAATTGGATGATAAACAATTGACAAATTGGATGATAAACAATTGACAAATTGGATGATAAACAATTGACAAATTGGATGATAAACAATTGACAAATTGGATGATAAACAATTGACAAATTGGATGATAAACAATTGACAAATTGGATAAACAATTGACAAATTGGATAAACAATTGACAAATTGGATAAATTGGATAAACAATTGACAAATTGGATAAACAATTGACAAATTGGATAAACAATTGGATAAACAATTGACAAATTGGATAAACAATTGACAAATTGGATAAATTGGATAAACAATTGACAAATTGGATAAACAATTGACAAATTGGATAAACAATTGACAAATTGGATAAACAATTGGATAAACAATTGGATAAACAATTGGATAAACAATTGGATAAACAATTGACAAACAA

FIG.\_4A

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- 721 GATCCGAATCTAATTGCGACAGTACACTATTACGGGTTTTTGGCCTTTTAGCGTGAÁTATC AspProAsnLeuIleAlaThrValHisTyrTyrGlyPheTrpProPheSerValAsnIle
- 781 GCCGGCTACACTCGCTTTGAAGAGGATTCGAAACGGGAGATCATCGAAACGTTTGATCGA AlaGlyTyrThrArgPheGluGluAspSerLysArgGluIleIleGluThrPheAspArg
- ValHisHisThrPheValAlaArgGlyIleProValValLeuGlyGluPheGlyLeuLeu
- 901 GGATTTGATAAACATACTGGAGTGATTCAACAAGGTGAAAAGCTAAAATTCTTTGAGTAT GlyPheAspLysHisThrGlyValIleGlnGlnGlyGluLysLeuLysPhePheGluTyr
- 961 CTCATCCATCATTTGAACGAGCGGGATATTACTCATATGCTTTGGGGATAATGGGCAGCAT LeuIleHisHisLeuAsnGluArgAspIleThrHisMetLeuTrpAspAsnGlyGlnHis
- 1021 TTCAATCGTCATACGTACGAATGGTATGACGAGGAATTGTTTGACATGTTGCGGGCAAGC PheAsnArgHisThrTyrGluTrpTyrAspGluGluLeuPheAspMetLeuArgAlaSer
- 1081 TGGGGAGGAAGATCATCCGTTGCAGAGTCGAACTTTATCTATTTAAAACAGGGAGACCGA TrpGlyGlyArgSerSerValAlaGluSerAsnPheIleTyrLeuLysGlnGlyAspArg
- 1141 ATCGCAGATGCAACAGTTACATTACAATTGCACGGAAATGAATTAACAGGGCTTCAGGCG IleAlaAspAlaThrValThrLeuGlnLeuHisGlyAsnGluLeuThrGlyLeuGlnAla
- 1201 AATGGACAACGACTAACGCCGGGGCAGGACTATGAGTTAAATGGAGAAAGACTTACAGTG AsnGlyGlnArgLeuThrProGlyGlnAspTyfGlùLeuAsnGlyGluArgLeuThrVal
- 1261 AAGGCCCATGTCCTATCGGCAATCGCAGGTTCAGGTACGTTAGGTACGAATGGAATGGTA LysAlaHisValLeuSerAlaIleAlaGlySerGiyThrLeuGlyThrAsnGlyMetVal
- 1321 ACGGCTGAGTTTAATCGTGGGGCAGATTGGCATTTTCGGGTGAATACGTATCGTACGCCT ThrAlaGluPheAsnArgGlyAlaAspTrpHisPheArgValAsnThrTyrArgThrPro
- 1381 GTATTGCAAAGCACGCAAGGTCACGTGAGCAACTTCAGCATTCCTGCTTCCTTTAATGGG ValLeuGlnSerThrGlnGlyHisValSerAsnPheSerIleProAlaSerPheAsnGly
- 1441 AATAGCTTAGCAACAATGGAGGCTGTCTATGTGGATGGCGGAAATGCTGGCCCGCAAGAC AsnSerLeuAlaThrMetGluAlaValTyrValAspGlyGlyAsnAlaGlyProGlnAsp
- TrpThrSerPheLysGluPheGlyTyrAlaPheSerProSerTyrAspThrHisGluIle
- 1561 AAACTGACCGAGGCGTTTTTTCGTGAGGTGCGGGATGGTGAAGTTCGGTTAACCTTCCAT LysLeuThrGluAlaPhePheArgGluValArgAspGlyGluValArgLeuThrPheHis
- 1621 TTTTGGAGŢĠGTGAAATAGTCAACTATACGATTATTAAAAACGGGAACCAGGTGACTGGG PheTrpSerGlyGluIleValAsnTyrThrIleIleLysAsnGlyAsnGlnValThrGly
- 1681 ATAGCAGCTCAGACAACCAATTCAAAAAACAAAAATAAAAAATGAAATTGAAAGCGCTTT IleAlaAlaGlnThrThrAsnSerLysAsnLysAsnLysLysEnd
- 1741 CTATGGTGTTGCCCGAATATCTGAGGTTCTTTAGTAGAATCCGATATTCGGGTTTTTTCA
- 1801 TACATTATAGGGGCGCTTTTTTATGTTGCGCAGGTTAAATGGTCTTACGTATGGGAACCC
- 1861 TACTACTAGATTATTGTGCACTCTTTTTGAGTACCATTATCACCGCCCTATCATATGTAT

FIG.\_4B

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- 1921 ATGAGTTGAACCATCTAGTAACCTCTCTTAAAATTGGTAAAGGAAATGTAACGTTGTGAT
- 2041 AGTAAGGAAATGGTATGATGGAGAGAGACGTGTGATCGAGAAATGGAGGAACGCAGAATG
- 2101 AATGAAACGATGCAACGCATCGCGAGAGTÇATAGAGAATGTGGAACGAGTGGCCGCCGGG
- 2161 AAACGTCAGGAAATCGAGCTGAGCCTTGTCGCATTATTTGCTAGCGG

FIG.\_4C